SEQUENCE LISTING

<110> MACK, DAVID
GISH, KURT

<120> NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST CANCER MODULATORS

<130> A-67860-3/DJB/JJD

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<141> 2000-03-15

<150> US 09/268,865
<151> 1999-03-15

<150> US 09/450,810
<151> 1999-11-29

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<151> 1999-12-02

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<170> PatentIn Ver. 2.1

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35 40 45

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Asp Tyr Thr Ala Thr Ile Tyr Leu Arg Gln Arg Trp Met Asp Gln Arg
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        115                 120                 125

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Ala Ser Ile Glu Ile Ser Ser Asp Asn Val Asp Tyr Ser Asp Leu Thr
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Arg Ile Val Asp Tyr Phe Thr Ile Gln Asn Pro Ser Asn Val Asp His
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<213> Homo sapiens

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Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu
    50                  55                  60

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65                  70                  75                  80

Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro
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Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser
            100                 105                 110

Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His
        115                 120                 125

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Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp
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Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu
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Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg
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<223> Description of Artificial Sequence: Synthetic

<400> 10
Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val Glu Tyr Cys
1 5 10 15

<210> 11
<211> 1958
<212> DNA
<213> Homo sapiens

<400> 11
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tccgctccgc tccgctcggc cccgcgccgc ccgtcaacat gatccgctgc ggcctggcct 120
gcgagcgctg ccgctggatc ctgcccctgc tcctactcag cgccatcgcc ttcgacatca 180
tcgcgctggc cggccgcggc tggttgcagt ctagcgacca cggccagacg tcctcgctgt 240
ggtggaaatg ctcccaagag ggcggcggca gcgggtccta cgaggagggc tgtcagagcc 300
tcatggagta cgcgtggggt agagcagcgg ctgccatgct cttctgtggc ttcatcatcc 360
tggtgatctg tttcatcctc tccttcttcg ccctctgtgg accccagatg cttgtcttcc 420
tgagagtgat tggaggtctc cttgccttgg ctgctgtgtt ccagatcatc tccctggtaa 480
tttaccccgt gaagtacacc cagaccttca cccttcatgc caaccctgct gtcacttaca 540
tctataactg ggcctacggc tttgggtggg cagccacgat tatcctgatt ggctgtgcct 600
tcttcttctg ctgcctcccc aactacgaag atgaccttct gggcaatgcc aagcccaggt 660
acttctacac atctgcctaa cttgggaatg aatgtgggag aaaatcgctg ctgctgagat 720
ggactccaga agaagaaact gtttctccag gcgactttga acccattttt tggcagtgtt 780
catattatta aactagtcaa aaatgctaaa ataatttggg agaaaatatt ttttaagtag 840
tgttatagtt tcatgtttat cttttattat gttttgtgaa gttgtgtctt ttcactaatt 900
acctatacta tgccaatatt tccttatatc tatccataac atttatacta catttgtaag 960
agaatatgca cgtgaaactt aacactttat aaggtaaaaa tgaggtttcc aagatttaat 1020
aatctgatca agttcttgtt atttccaaat agaatggact cggtctgtta agggctaagg 1080
agaagaggaa gataaggtta aaagttgtta atgaccaaac attctaaaag aaatgcaaaa 1140
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atatcatttg tgagaatttc tcattaatat cctgaatcat tcattttagc taaggcttca 1260
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atgttcagaa ccagagtaga ctggattgaa agatggactg ggtctaattt atcatgactg 1500
atagatctgg ttaagttgtg tagtaaagca ttaggagggt cattcttgtc acaaaagtgc 1560
cactaaaaca gcctcaggag aataaatgac ttgcttttct aaatctcagg tttatctggg 1620

ctctatcata tagacaggct tctgatagtt tgcaactgta agcagaaacc tacatatagt 1680
taaaatcctg gtctttcttg gtaaacagat tttaaatgtc tgatataaaa catgccacag 1740
gagaattcgg ggatttgagt ttctctgaat agcatatata tgatgcatcg gataggtcat 1800
tatgattttt taccatttcg acttacataa tgaaaaccaa ttcattttaa atatcagatt 1860
attattttgt aagttgtgga aaaagctaat tgtagttttc attatgaagt tttcccaata 1920
aaccaggtat tctaaacttg aaaaaaaaaa aaaaaaaa 1958

<210> 12
<211> 582
<212> DNA
<213> Homo sapiens

<400> 12
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agcgccatcg ccttcgacat catcgcgctg gccggccgcg gctggttgca gtctagcgac 120
cacggccaga cgtcctcgct gtggtggaaa tgctcccaag agggcggcgg cagcgggtcc 180
tacgaggagg gctgtcagag cctcatggag tacgcgtggg gtagagcagc ggctgccatg 240
ctcttctgtg gcttcatcat cctggtgatc tgtttcatcc tctccttctt cgccctctgt 300
ggaccccaga tgcttgtctt cctgagagtg attggaggtc tccttgcctt ggctgctgtg 360
ttccagatca tctccctggt aatttacccc gtgaagtaca cccagacctt caccttcat 420
gccaaccctg ctgtcactta catctataac tgggcctacg gctttgggtg ggcagccacg 480
attatcctga ttggctgtgc cttcttcttc tgctgcctcc ccaactacga agatgacctt 540
ctgggcaatg ccaagcccag gtacttctac acatctgcct aa 582

<210> 13
<211> 193
<212> PRT
<213> Homo sapiens

<400> 13
Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
1 5 10 15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
20 25 30

Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
35 40 45

Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met
65 70 75 80

Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
85 90 95

Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly

```
            100                 105                 110

Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Leu Ser Leu Val Ile
        115                 120                 125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala
    130                 135                 140

Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145                 150                 155                 160

Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
                165                 170                 175

Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
            180                 185                 190

Ala
```

<210> 14
<211> 193
<212> PRT
<213> Mouse

<400> 14

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Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
  1               5                  10                  15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
             20                  25                  30

Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
         35                  40                  45

Trp Arg Cys Phe Asp Glu Gly Gly Gly Ser Gly Ser Tyr Asp Asp Gly
     50                  55                  60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr
 65                  70                  75                  80

Leu Phe Cys Gly Phe Ile Ile Leu Cys Ile Cys Phe Ile Leu Ser Phe
                 85                  90                  95

Phe Ala Leu Cys Gly Pro Met Gln Leu Val Phe Leu Arg Val Ile Gly
            100                 105                 110

Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Leu Ser Leu Val Ile
        115                 120                 125
```

```
Tyr Pro Val Lys Tyr Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala
    130                 135                 140

Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145                 150                 155                 160

Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr
                165                 170                 175

Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
            180                 185                 190

Ala
```

<210> 15
<211> 124
<212> PRT
<213> Rat

<400> 15

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Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr Leu Phe Cys Gly Phe
  1               5                  10                  15

Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly
             20                  25                  30

Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu
         35                  40                  45

Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr
     50                  55                  60

Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr
 65                  70                  75                  80

Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly
                 85                  90                  95

Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu
            100                 105                 110

Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala
        115                 120
```

<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 16
Cys Ser Tyr Ser Ala Pro Ser Pro Ser Thr Ser Ser Arg Trp Pro
1 5 10 15

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 17
Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro
1 5 10 15

<210> 18
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 18
Cys Gly Gly Asn Ala Pro Lys Arg Gly Gly Gly Arg Gly Ser Tyr
1 5 10 15

<210> 19
<211> 1970
<212> DNA
<213> Mouse

<400> 19
gtcaccggaa tcaaggtgtg gctggagcgc cgctcccccg ccgycagccc gkkggccgcg 60
tcttcggggg agccgcctct tccttwattc ggckcygaca gcgctcgcag gaccactctt 120
ggccgctgct cctgcccggc gttcctccgc tccgcgcccg ccgccaccga cgacatgctg 180
cgctgcggcc tggcctgcga gcgctgcagg tggatcctgc ccctgctgct gctcagcgcc 240
atcgccttcg acatcatcgc gctggccggc cgcggctggc tgcagtctag caaccacatc 300
cagacatcgt cgctttggtg gaggtgtttc gacgagggcg gcggcagcgg ctcctacgac 360
gatggctgcc agagcctcat ggagtacgca tggggacgag cagctgcagc cacgcttttc 420
tgtggcttta tcatcctgtg catctgcttc attctctcgt tcttcgccct gtgtggaccc 480
cagatgcttg ttttcctgag agtcattgga ggcctcctcg cactggctgc catattccag 540
atcatctccc tggtaatcta ccccgtgaag tacacacaga ccttcaggct tcacgataac 600
cctgctgtta attacatcta taactgggcc tatggcttcg gatgggcggc caccatcatc 660

ttgattggtt gttccttctt cttctgctgc ctccccaact acgaggatga ccttttgggg 720
gccgccaagc ccaggtactt ctatccccca gcctaatgtg ggaggaagag cctgagaaaa 780
gcctgctgca agatggatct gaggaggaaa ctgttctcca aggcacaagg aacctacgtt 840
tgggcaatgt tcatatgatc agaaatgtta gaataaatgc taaagaaaat tcttcataat 900
tagtgttaag tttcatgtat gtcgtgtgga gttaaaaaga cttgaattct gtttgctaag 960
tatatgctaa tttttcctta tgtcaattct ataccattta agcttcattt gttaaagaat 1020
atgcctgtga aacttgataa ggtagaaatg gagcagcctc tcatttaata atctgatggg 1080
gcttctgttt ttccacatag aatgggttgt ttctgctaag ggctacagag gaggaaagtc 1140
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tattttgagt tttcagttac ataaagaagc agaagcagat tggtttccta agtgagcatc 1260
atttgtgaga atttttagtc agtgttttga acaattattg tttttctaag cttcatgttg 1320
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tgaaatgcta agaattttcc tcttttcccg tagtgtagag gggtagggtg tgggcagaag 1440
ccgtgttagc acatctgtag tattgtgtgt gtatgcttag aaccagcgta gaccggatgg 1500
gaggatggac taggcctaat ccctcccaac tggtggatgt gaagaggtca ggtaggaagg 1560
cacaggaggg tcaccactgt cacagcagtg ccatgcagac atcctaggag aagacatggc 1620
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attttaactg aaacagaaac ctaaatgtaa ttaaaaacct ggtcttcctt ggtaagcaga 1740
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ataccggaag ggctactatt acctttttct taccatttat acttacctaa tggaaacgag 1860
cttgttttaa ctatcagaac actattttgt aaggtgctgc aaagacagtt gaagttttca 1920
ttaccaattt ccccaataaa ccaggtgttc aaatcctgaa aaaaaaaggc 1970

<210> 20
<211> 582
<212> DNA
<213> Mouse

<400> 20
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agcgccatcg ccttcgacat catcgcgctg gccggccgcg gctggctgca gtctagcaac 120
cacatccaga catcgtcgct ttggtggagg tgtttcgacg agggcggcgg cagcggctcc 180
tacgacgatg gctgccagag cctcatggag tacgcatggg gacgagcagc tgcagccacg 240
cttttctgtg gctttatcat cctgtgcatc tgcttcattc tctcgttctt cgccctgtgt 300
ggaccccaga tgcttgtttt cctgagagtc attggaggcc tcctcgcact ggctgccata 360
ttccagatca tctccctggt aatctacccc gtgaagtaca cacagacctt caggcttcac 420
gataaccctg ctgttaatta catctataac tgggcctatg gcttcggatg ggcggccacc 480
atcatcttga ttggttgttc cttcttcttc tgctgcctcc ccaactacga ggatgacctt 540
ttgggggccg ccaagcccag gtacttctat cccccagcct aa 582

<210> 21
<211> 536
<212> DNA
<213> Rat

<400> 21
gaatacgcct ggggccgagc agctgctgcc actctcttct gtggattcat catcctggtc 60
atctgcttca tcctctcgtt cttcgccctg tgtggacccc agatgcttgt tttcctgaga 120
gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct ggttatctat 180

cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240
aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctctttcttc 300
ttctgctgcc tccccaacta cgaggatgac cttctgggca atgcaaagcc caggtacttc 360
tatacatctg cctaatgtgg agggagatcc tgagaaaagc ctgctgcaag atgcatgtga 420
ggaggaaagt gttctccaag gagcaaagaa cctatgtttg ggcagtgttc atatgagtgg 480
aaatgctaga ataaatgcta aagaaaattc ttcataaaaa aaaaaaaaaa aaaaaa 536

<210> 22
<211> 375
<212> DNA
<213> Rat

<400> 22
gaatacgcct ggggccgagc agctgctgcc actctcttct gtggattcat catcctggtc 60
atctgcttca tcctctcgtt cttcgccctg tgtggacccc agatgcttgt tttcctgaga 120
gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct ggttatctat 180
cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240
aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctctttcttc 300
ttctgctgcc tccccaacta cgaggatgac cttctgggca atgcaaagcc caggtacttc 360
tatacatctg cctaa 375

<210> 23
<211> 471
<212> DNA
<213> Homo sapiens

<400> 23
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agtcctggta ctcttgggag tttccatctt tctggtctct gcccagaatc cgacaacagc 120
tgctccagct gacacgtatc cagctactgg tcctgctgat gatgaagccc ctgatgctga 180
aaccactgct gctgcaacaa ctgcgaccac tgctgctcct accactgcaa ccaccgctgc 240
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tggtagagtg tgtccctgag atggaatcag cttgagtctt ctgcaattgg gtcacaacta 360
ttcatgcttc ctgtgatttc atccaactac ttaccttgcc tacgatatcc cctttatctc 420
taatcagttt attttctttc aaataaaaaa taactatgag cgagctaaca t 471

<210> 24
<211> 273
<212> DNA
<213> Homo sapiens

<400> 24
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aatccgacaa cagctgctcc agctgacacg tatccagcta ctggtcctgc tgatgatgaa 120
gcccctgatg ctgaaaccac tgctgctgca accactgcga ccactgctgc tcctaccact 180
gcaaccaccg ctgcttctac cactgctcgt aaagacattc cagttttacc caaatgggtt 240
ggggatctcc cgaatggtag agtgtgtccc tga 273

<210> 25
<211> 90
<212> PRT
<213> Homo sapiens

<400> 25
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 26
Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro Ala Cys
1 5 10 15

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 27
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
1 5 10 15

<210> 28
<211> 1555
<212> DNA
<213> Homo sapiens

<400> 28
ggagttttct ggagctgttg caatgtgtat gctggtgaaa tctacttgag cattaagcag 60
tatctcccag cattgttagc tactgagtgg cacatcttca gtacgcatga ttcgtggggg 120
actcaggcag aggtaaaagt gtgaaacttt tcagcattac ctaagaagca aaggctcaat 180
tttggctgct tcattcttat ctcttctgcc acagttctaa cgtgcctgat ctactgagac 240
caaggatgac caatgactca gaagggaaaa tgggatttaa acacccaaag atcatgggga 300
atttcagagg tcatgccctc cctggaacct tctttttat tattggtctt tggtggtgta 360
caaagagtat tctgaagtat atctgcaaaa agcaaaagcg aacctgctat cttggttcca 420
aaacattatt ctatcgattg gaaattttgg agggaattac aatagttggc atggctttaa 480
ctggcatggc tggggagcag tttattcctg gagggcccca tctgatgtta tatgactata 540
aacaaggtca ctggaatcaa ctcctgggct ggcatcattt caccatgtat ttcttctttg 600
ggctgttggg tgtggcagat atcttatgtt tcaccatcag ttcacttcct gtgtccttaa 660
ccaagttaat gttgtcaaat gccttatttg tggaggcctt tatcttctac aaccacactc 720
atggccggga aatgctggac atctttgtgc accagctgct ggttttggtc gtctttctga 780
caggcctcgt tgccttccta gagttccttg ttcggaacaa tgtacttctg gagctattgc 840
ggtcaagtct cattctgctt caggggagct ggttctttca gattggattt gtcctgtatc 900
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aaaatgctga acgagaacaa gaatcagaag aagaaatgtg actttgatga gcttccagtt 1140
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tggagaacag ctggctaagg atgactctaa gtgtactgtt tgcatttcca atttggttaa 1260
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aaagttggat gcccacacta tgaaagaaat atttgtttta tttgccttat agatatgctc 1440
aaggttactg ggcttgctac tatttgtaac tccttgacca tggaattata cttgtttatc 1500
ttgttgctgc aatgagaaat aaatgaatgt atgtattttg gtgcagaaaa aaaaa 1555

<210> 29
<211> 291
<212> PRT
<213> Homo sapiens

<400> 29
Met Thr Asn Asp Ser Glu Gly Lys Met Gly Phe Lys His Pro Lys Ile
1 5 10 15

Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
20 25 30

Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
35 40 45

Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
50 55 60

Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
65 70 75 80

Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
85 90 95

Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
100 105 110

Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
115 120 125

Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser
130 135 140

Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly
145 150 155 160

Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val
165 170 175

Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn
180 185 190

Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser
195 200 205

Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro
210 215 220

Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys
225 230 235 240

Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr
245 250 255

Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser
260 265 270

Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
275 280 285

Glu Glu Met
290

<210> 30
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 30
Tyr Pro Pro Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Cys
1 5 10 15

<210> 31
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 31
Cys Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu Glu Glu Met
1 5 10 15

<210> 32
<211> 10320
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (10123)..(10185)
<223> "n" at positions 10123 and 10185 can be any base.

<400> 32
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gcggagactg aggtcctgac aagcgataac atttctgata aagacccgat cttactgcaa 120
tctctagcgt cctcttttt ggtgctgctg gtttctccag acctcgcgtc ctctcgattg 180
ctctctcgcc ttcctatttc ttttttttt ttttaaacaa aaaacaacac cccctcccct 240
ctcccacccg gcaccgggca catccttgct ctatttcctt tctctttctc tctctctctc 300
tctctctctc ttttttaata agggtggggg agggaaaggg gggggatgca ggaaagacct 360
ttttctctcc cccccgcaat aatccaagat caactctgca aacaacagaa gacggttcat 420
ggctttggcc gccgcgccac catctttcgg gctgccgagg gtgttcttga cgattaatca 480
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Gly Val Leu Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly
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Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys
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His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser
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Ser Glu Val Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro
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Tyr Tyr Trp Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser
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Lys Thr Asp Lys Ser Ser Ser Gly Ala Lys Lys Lys Asp Phe Ser Ser
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Val Ser Gly Thr Gln Glu Gln Thr Lys Thr Leu Arg Asp Ser Pro Asn
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Val Glu Ala Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu
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<212> DNA
<213> Homo sapiens

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<210> 35
<211> 871
<212> PRT
<213> Homo sapiens

<400> 35
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Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
20 25 30

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Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
         35                  40                  45

Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
     50                  55                  60

Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
 65                  70                  75                  80

Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
                 85                  90                  95

Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
            100                 105                 110

Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
        115                 120                 125

Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
    130                 135                 140

Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
145                 150                 155                 160

Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
                165                 170                 175

Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
            180                 185                 190

Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
        195                 200                 205

Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
    210                 215                 220

His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225                 230                 235                 240

Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
                245                 250                 255

Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
            260                 265                 270

Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
        275                 280                 285

Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
    290                 295                 300
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Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305                 310                 315                 320

Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
                325                 330                 335

Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
            340                 345                 350

Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
        355                 360                 365

Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
    370                 375                 380

Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385                 390                 395                 400

Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
                405                 410                 415

Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
            420                 425                 430

Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
        435                 440                 445

Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
    450                 455                 460

Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465                 470                 475                 480

Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
                485                 490                 495

Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
            500                 505                 510

Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
        515                 520                 525

Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
    530                 535                 540

Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
545                 550                 555                 560

Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
                565                 570                 575
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His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
580 585 590

Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
595 600 605

Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
610 615 620

Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
625 630 635 640

Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
645 650 655

Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
660 665 670

Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
675 680 685

Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
690 695 700

Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
705 710 715 720

Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
725 730 735

Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
740 745 750

His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
755 760 765

Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
770 775 780

Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
785 790 795 800

Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
805 810 815

Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
820 825 830

Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
835 840 845

Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
850 855 860

Leu Trp Asp Gly Trp Glu Gly
865 870

<210> 36
<211> 1922
<212> DNA
<213> Homo sapiens

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aa 1922

<210> 37
<211> 1179
<212> DNA

<213> Homo sapiens

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<210> 38
<211> 392
<212> PRT
<213> Homo sapiens

<220>
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<222> (111)
<223> "Xaa" at position 111 can be any amino acid.

<400> 38
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Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
20 25 30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
35 40 45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
50 55 60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
65 70 75 80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
85 90 95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
100 105 110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
115 120 125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
130 135 140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145 150 155 160

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
165 170 175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
180 185 190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
195 200 205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
210 215 220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225 230 235 240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
245 250 255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
260 265 270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
275 280 285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
290 295 300

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305 310 315 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
325 330 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
340 345 350

```
Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
        355                 360                 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370                 375                 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385                 390
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<210> 39
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (111)
<223> "Xaa" at position 111 can be any amino acid.

<400> 39

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  1               5                  10                  15

Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
             20                  25                  30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
         35                  40                  45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
     50                  55                  60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65                  70                  75                  80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
                 85                  90                  95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
            100                 105                 110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
        115                 120                 125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
    130                 135                 140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145                 150                 155                 160
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```
Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
                165                 170                 175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
            180                 185                 190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
        195                 200                 205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
    210                 215                 220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225                 230                 235                 240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
                245                 250                 255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
            260                 265                 270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
        275                 280                 285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
    290                 295                 300

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305                 310                 315                 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
                325                 330                 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
            340                 345                 350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
        355                 360                 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370                 375                 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385                 390
```

<210> 40
<211> 162
<212> PRT
<213> Mouse

<400> 40
Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu Ile Val Val Pro Glu
1 5 10 15

Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu Val Met Arg
20 25 30

Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr Cys Gln Thr
35 40 45

Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys Leu Trp Ile
50 55 60

Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe Gln Val Pro
65 70 75 80

Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val
85 90 95

Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
100 105 110

Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala His Pro Gln
115 120 125

Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met Phe Pro Arg
130 135 140

Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe Leu Arg Pro
145 150 155 160

Tyr Lys

<210> 41
<211> 2840
<212> DNA
<213> Homo sapiens

<400> 41
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acaaccacag ctggcccgaa agcctggcct gcgacgagct gcctgtctat gaccgtggcg 660
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tcacaccaga catgatggta caggaaaggc ctcttgatgt tgactgtaaa cgcctaagcc 780
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tcccgctcat tacaaattct tcttgccagt gtccacacat cctgccccat caagatgttc 1020
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cctatctaat cctactctcc actacacaga ggtaatcact attagtattt tggcatatta 2580
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gtatacatgt gtttcataac ctgcctcctt tgcttggccc tttattgaga taagttttcc 2700
tgtcaagaaa gcagaaacca tctcatttct aacagctgtg ttatattcca tagtatgcat 2760
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taaacatctc accggaattc 2840

<210> 42
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 42
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cggatgccca accacctgca ccacagcacg caggagaacg ccatcctggc catcgagcag 180
tacgaggagc tggtggacgt gaactgcagc gccgtgctgc gcttcttctt ctgtgccatg 240
tacgcgccca tttgcaccct ggagttcctg cacgacccta tcaagccgtg caagtcggtg 300

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tgccaacgcg cgcgcgacga ctgcgagccc ctcatgaaga tgtacaacca cagctggccc 360
gaaagcctgg cctgcgacga gctgcctgtc tatgaccgtg gcgtgtgcat ttcgcctgaa 420
gccatcgtca cggacctccc ggaggatgtt aagtggatag acatcacacc agacatgatg 480
gtacaggaaa ggcctcttga tgttgactgt aaacgcctaa gccccgatcg gtgcaagtgt 540
aaaaaggtga agccaacttt ggcaacgtat ctcagcaaaa actacagcta tgttattcat 600
gccaaaataa aagctgtgca gaggagtggc tgcaatgagg tcacaacggt ggtggatgta 660
aaagagatct tcaagtcctc atcacccatc cctcgaactc aagtcccgct cattacaaat 720
tcttcttgcc agtgtccaca catcctgccc catcaagatg ttctcatcat gtgttacgag 780
tggcgttcaa ggatgatgct tcttgaaaat tgcttagttg aaaaatggag agatcagctt 840
agtaaaagat ccatacagtg ggaagagagg ctgcaggaac agcggagaac agttcaggac 900
aagaagaaaa cagccgggcg caccagtcgt agtaatcccc ccaaaccaaa gggaaagcct 960
cctgctccca aaccagccag tcccaagaag aacattaaaa ctaggagtgc ccagaagaga 1020
acaaacccga aaagagtgtg a                                          1041
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<210> 43
<211> 346
<212> PRT
<213> Homo sapiens

<400> 43

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Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
  1               5                  10                  15

Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
             20                  25                  30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
         35                  40                  45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
     50                  55                  60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
 65                  70                  75                  80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
                 85                  90                  95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
            100                 105                 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
        115                 120                 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
    130                 135                 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
145                 150                 155                 160
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Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
                165                 170                 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
            180                 185                 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
        195                 200                 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
    210                 215                 220

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
225                 230                 235                 240

Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
                245                 250                 255

Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
            260                 265                 270

Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
        275                 280                 285

Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
    290                 295                 300

Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
305                 310                 315                 320

Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
                325                 330                 335

Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
            340                 345
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<210> 44
<211> 749
<212> DNA
<213> Homo sapiens

<400> 44
cggcaccaag agcactggcc aagtcagctt cttctgagag agtctctaga agacatgatg 60
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gcaataaaaa aggaaaagag gcctcctcag acactctcaa gaggatgggg agatgacatc 180
acttgggtac aaacttatga agaaggtctc ttttatgctc aaaaaagtaa gaagccatta 240
atggttattc atcacctgga ggattgtcaa tactctcaag cactaaagaa agtatttgcc 300
caaaatgaag aaatacaaga aatggctcag aataagttca tcatgctaaa ccttatgcat 360
gaaaccactg ataagaattt atcacctgat gggcaatatg tgcctagaat catgtttgta 420
gacccttctt taacagttag agctgacata gctggaagat actctaacag attgtacaca 480

tatgagcctc gggatttacc cctattgata gaaaacatga agaaagcatt aagacttatt 540
cagtcagagc tataagagat gatagaaaaa agccttcact tcaaagaagt caaatttcat 600
gaagaaaacc tctggcacat tgacaaatac taaatgtgca agtatataga ttttgtaata 660
ttactattta gttttttaa tgtgtttgca atagtcttat taaaataaat gttttttaaa 720
tctgaaaaaa aaaaaaaaaa aaaaaaaaa 749

<210> 45
<211> 501
<212> DNA
<213> Homo sapiens

<400> 45
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gacatcactt gggtacaaac ttatgaagaa ggtctctttt atgctcaaaa aagtaagaag 180
ccattaatgg ttattcatca cctggaggat tgtcaatact ctcaagcact aaagaaagta 240
tttgcccaaa atgaagaaat acaagaaatg gctcagaata agttcatcat gctaaacctt 300
atgcatgaaa ccactgataa gaatttatca cctgatgggc aatatgtgcc tagaatcatg 360
tttgtagacc cttctttaac agttagagct gacatagctg gaagatactc taacagattg 420
tacacatatg agcctcggga tttaccccta ttgatagaaa acatgaagaa agcattaaga 480
cttattcagt cagagctata a 501

<210> 46
<211> 166
<212> PRT
<213> Homo sapiens

<400> 46
Met Met Leu His Ser Ala Leu Gly Leu Cys Leu Leu Leu Val Thr Val
1 5 10 15

Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro Pro Gln
20 25 30

Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln Thr Tyr
35 40 45

Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu Met Val
50 55 60

Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys Lys Val
65 70 75 80

Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys Phe Ile
85 90 95

Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser Pro Asp
100 105 110

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Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val
        115                 120                 125

Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu
    130                 135                 140

Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala Leu Arg
145                 150                 155                 160

Leu Ile Gln Ser Glu Leu
                165
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<210> 47
<211> 3493
<212> DNA
<213> Homo sapiens

<400> 47

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taaagtactc tcgctggtat tgtcagtatg tgtgttaaca acaatacttg gttgtatatt 300
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tagcaaacta aaaaaatgtg gaacatatac taaaaacatg agaccggtat atccaacaaa 780
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<210> 48
<211> 925
<212> PRT
<213> Homo sapiens

<400> 48
Met Glu Arg Asp Gly Cys Ala Gly Gly Gly Ser Arg Gly Gly Glu Gly
1 5 10 15

Gly Arg Ala Pro Arg Glu Gly Pro Ala Gly Asn Gly Arg Asp Arg Gly
20 25 30

Arg Ser His Ala Ala Glu Ala Pro Gly Asp Pro Gln Ala Ala Ala Ser
35 40 45

Leu Leu Ala Pro Met Asp Val Gly Glu Glu Pro Leu Glu Lys Ala Ala
50 55 60

Arg Ala Arg Thr Ala Lys Asp Pro Asn Thr Tyr Lys Val Leu Ser Leu
65 70 75 80

Val Leu Ser Val Cys Val Leu Thr Thr Ile Leu Gly Cys Ile Phe Gly

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                85                  90                  95

Leu Lys Pro Ser Cys Ala Lys Glu Val Lys Ser Cys Lys Gly Arg Cys
            100                 105                 110

Phe Glu Arg Thr Phe Gly Asn Cys Arg Cys Asp Ala Ala Cys Val Glu
        115                 120                 125

Leu Gly Asn Cys Cys Leu Asp Tyr Gln Glu Thr Cys Ile Glu Pro Glu
    130                 135                 140

His Ile Trp Thr Cys Asn Lys Phe Arg Cys Gly Glu Lys Arg Leu Thr
145                 150                 155                 160

Arg Ser Leu Cys Ala Cys Ser Asp Asp Cys Lys Asp Lys Gly Asp Cys
                165                 170                 175

Cys Ile Asn Tyr Ser Ser Val Cys Gln Gly Glu Lys Ser Trp Val Glu
            180                 185                 190

Glu Pro Cys Glu Ser Ile Asn Glu Pro Gln Cys Pro Ala Gly Phe Glu
        195                 200                 205

Thr Pro Pro Thr Leu Leu Phe Ser Leu Asp Gly Phe Arg Ala Glu Tyr
    210                 215                 220

Leu His Thr Trp Gly Gly Leu Leu Pro Val Ile Ser Lys Leu Lys Lys
225                 230                 235                 240

Cys Gly Thr Tyr Thr Lys Asn Met Arg Pro Val Tyr Pro Thr Lys Thr
                245                 250                 255

Phe Pro Asn His Tyr Ser Ile Val Thr Gly Leu Tyr Pro Glu Ser His
            260                 265                 270

Gly Ile Ile Asp Asn Lys Met Tyr Asp Pro Lys Met Asn Ala Ser Phe
        275                 280                 285

Ser Leu Lys Ser Lys Glu Lys Phe Asn Pro Glu Trp Tyr Lys Gly Glu
    290                 295                 300

Pro Ile Trp Val Thr Ala Lys Tyr Gln Gly Leu Lys Ser Gly Thr Phe
305                 310                 315                 320

Phe Trp Pro Gly Ser Asp Val Glu Ile Asn Gly Ile Phe Pro Asp Ile
                325                 330                 335

Tyr Lys Met Tyr Asn Gly Ser Val Pro Phe Glu Glu Arg Ile Leu Ala
            340                 345                 350

Val Leu Gln Trp Leu Gln Leu Pro Lys Asp Glu Arg Pro His Phe Tyr
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        355                 360                 365

Thr Leu Tyr Leu Glu Glu Pro Asp Ser Ser Gly His Ser Tyr Gly Pro
    370                 375                 380

Val Ser Ser Glu Val Ile Lys Ala Leu Gln Arg Val Asp Gly Met Val
385                 390                 395                 400

Gly Met Leu Met Asp Gly Leu Lys Glu Leu Asn Leu His Arg Cys Leu
                405                 410                 415

Asn Leu Ile Leu Ile Ser Asp His Gly Met Glu Gln Gly Ser Cys Lys
            420                 425                 430

Lys Tyr Ile Tyr Leu Asn Lys Tyr Leu Gly Asp Val Lys Asn Ile Lys
        435                 440                 445

Val Ile Tyr Gly Pro Ala Ala Arg Leu Arg Pro Ser Asp Val Pro Asp
    450                 455                 460

Lys Tyr Tyr Ser Phe Asn Tyr Glu Gly Ile Ala Arg Asn Leu Ser Cys
465                 470                 475                 480

Arg Glu Pro Asn Gln His Phe Lys Pro Tyr Leu Lys His Phe Leu Pro
                485                 490                 495

Lys Arg Leu His Phe Ala Lys Ser Asp Arg Ile Glu Pro Leu Thr Phe
            500                 505                 510

Tyr Leu Asp Pro Gln Trp Gln Leu Ala Leu Asn Pro Ser Glu Arg Lys
        515                 520                 525

Tyr Cys Gly Ser Gly Phe His Gly Ser Asp Asn Val Phe Ser Asn Met
    530                 535                 540

Gln Ala Leu Phe Val Gly Tyr Gly Pro Gly Phe Lys His Gly Ile Glu
545                 550                 555                 560

Ala Asp Thr Phe Glu Asn Ile Glu Val Tyr Asn Leu Met Cys Asp Leu
                565                 570                 575

Leu Asn Leu Thr Pro Ala Pro Asn Asn Gly Thr His Gly Ser Leu Asn
            580                 585                 590

His Leu Leu Lys Asn Pro Val Tyr Thr Pro Lys His Pro Lys Glu Val
        595                 600                 605

His Pro Leu Val Gln Cys Pro Phe Thr Arg Asn Pro Arg Asp Asn Leu
    610                 615                 620

Gly Cys Ser Cys Asn Pro Ser Ile Leu Pro Ile Glu Asp Phe Gln Thr
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625 630 635 640

Gln Phe Asn Leu Thr Val Ala Glu Glu Lys Ile Ile Lys His Glu Thr
645 650 655

Leu Pro Tyr Gly Arg Pro Arg Val Leu Gln Lys Glu Asn Thr Ile Cys
660 665 670

Leu Leu Ser Gln His Gln Phe Met Ser Gly Tyr Ser Gln Asp Ile Leu
675 680 685

Met Pro Leu Trp Thr Ser Tyr Thr Val Asp Arg Asn Asp Ser Phe Ser
690 695 700

Thr Glu Asp Phe Ser Asn Cys Leu Tyr Gln Asp Phe Arg Ile Pro Leu
705 710 715 720

Ser Pro Val His Lys Cys Ser Phe Tyr Lys Asn Asn Thr Lys Val Ser
725 730 735

Tyr Gly Phe Leu Ser Pro Pro Gln Leu Asn Lys Asn Ser Ser Gly Ile
740 745 750

Tyr Ser Glu Ala Leu Leu Thr Thr Asn Ile Val Pro Met Tyr Gln Ser
755 760 765

Phe Gln Val Ile Trp Arg Tyr Phe His Asp Thr Leu Leu Arg Lys Tyr
770 775 780

Ala Glu Glu Arg Asn Gly Val Asn Val Val Ser Gly Pro Val Phe Asp
785 790 795 800

Phe Asp Tyr Asp Gly Arg Cys Asp Ser Leu Glu Asn Leu Arg Gln Lys
805 810 815

Arg Arg Val Ile Arg Asn Gln Glu Ile Leu Ile Pro Thr His Phe Phe
820 825 830

Ile Val Leu Thr Ser Cys Lys Asp Thr Ser Gln Thr Pro Leu His Cys
835 840 845

Glu Asn Leu Asp Thr Leu Ala Phe Ile Leu Pro His Arg Thr Asp Asn
850 855 860

Ser Glu Ser Cys Val His Gly Lys His Asp Ser Ser Trp Val Glu Glu
865 870 875 880

Leu Leu Met Leu His Arg Ala Arg Ile Thr Asp Val Glu His Ile Thr
885 890 895

Gly Leu Ser Phe Tyr Gln Gln Arg Lys Glu Pro Val Ser Asp Ile Leu

900 905 910

Lys Leu Lys Thr His Leu Pro Thr Phe Ser Gln Glu Asp
915 920 925

<210> 49
<211> 2709
<212> DNA
<213> Homo sapiens

<400> 49
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tgctctgtca tatatttact aattgtatgg ctgggaccaa aatacatgag gaataaacag 180
ccattctctt gccgggggat tttagtggtg tataaccttg gactcacact gctgtctctg 240
tatatgttct gtgagttagt aacaggagta tgggaaggca aatacaactt cttctgtcag 300
ggcacacgca ccgcaggaga atcagatatg aagattatcc gtgtcctctg gtggtactac 360
ttctccaaac tcatagaatt tatggacact ttcttcttca tcctgcgcaa gaacaaccac 420
cagatcacgg tcctgcacgt ctaccaccat gcctcgatgc tgaacatctg gtggtttgtg 480
atgaactggg tcccctgcgg ccactcttat tttggtgcca cacttaatag cttcatccac 540
gtcctcatgt actcttacta tggtttgtcg tcagtccctt ccatgcgtcc atacctctgg 600
tggaagaagt acatcactca ggggcagctg cttcagtttg tgctgacaat catccagacc 660
agctgcgggg tcatctggcc gtgcacattc cctcttggtt ggttgtattt ccagattgga 720
tacatgattt ccctgattgc tctcttcaca aacttctaca ttcagaccta caacaagaaa 780
ggggcctccc gaaggaaaga ccacctgaag gaccaccaga atgggtccat ggctgctgtg 840
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aaggattgaa gtcaaagaat tgaaaccctc caaaccacgt catctgattg taagcacaat 960
atgagttgtg ccccaatgct cgttaacagc tgctgtaact agtctggcct acaatagtgt 1020
gattcatgta ggacttcttt catcaattca aaacccctag aaaacgtata cagattatat 1080
aagtagggat aagatttcta acatttctgg gctctctgac ccctgcgcta gactgtggaa 1140
agggagtatt attatagtat acaacactgc tgttgcctta ttagttataa catgataggt 1200
gctgaattgt gattcacaat ttaaaaacac tgtaatccaa actttttttt ttaactgtag 1260
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ttgtactatt ggctttgaat caagcaggct caaatctagt ggaacagtca gtttaacttt 1560
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gcctagttta ccaaaattaa caaaggggg gaaaggacct tagaactttt taaggtaaaa 1980
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ttgacaatgt ataaactaat tgttggtttg atatttatgt aaatatcagt ttaccatgct 2340

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tctgtttgaa aaggagtcat ggcatctgtt tacatttacc ttatcaaacc tagaatgtgt 2460
atatttataa atgtatgtct tcattgctag gtactaattt gcagatgtct ttacatattt 2520
caatacagaa actataacat tcaatagtgt gctgtcaaag tgtgcttagc tcacctggat 2580
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700
aaaaaaaaa 2709

<210> 50
<211> 299
<212> PRT
<213> Homo sapiens

<400> 50
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Gly Pro Arg Asp Thr Arg Val Lys Gly Trp Phe Leu Leu Asp Asn Tyr
20 25 30

Ile Pro Thr Phe Ile Cys Ser Val Ile Tyr Leu Leu Ile Val Trp Leu
35 40 45

Gly Pro Lys Tyr Met Arg Asn Lys Gln Pro Phe Ser Cys Arg Gly Ile
50 55 60

Leu Val Val Tyr Asn Leu Gly Leu Thr Leu Leu Ser Leu Tyr Met Phe
65 70 75 80

Cys Glu Leu Val Thr Gly Val Trp Glu Gly Lys Tyr Asn Phe Phe Cys
85 90 95

Gln Gly Thr Arg Thr Ala Gly Glu Ser Asp Met Lys Ile Ile Arg Val
100 105 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe
115 120 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Val Leu His Val
130 135 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
145 150 155 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe Ile
165 170 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser Met
180 185 190

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Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Gly Gln Leu Leu
        195                 200                 205

Gln Phe Val Leu Thr Ile Ile Gln Thr Ser Cys Gly Val Ile Trp Pro
    210                 215                 220

Cys Thr Phe Pro Leu Gly Trp Leu Tyr Phe Gln Ile Gly Tyr Met Ile
225                 230                 235                 240

Ser Leu Ile Ala Leu Phe Thr Asn Phe Tyr Ile Gln Thr Tyr Asn Lys
                245                 250                 255

Lys Gly Ala Ser Arg Arg Lys Asp His Leu Lys Asp His Gln Asn Gly
            260                 265                 270

Ser Met Ala Ala Val Asn Gly His Thr Asn Ser Phe Ser Pro Leu Glu
        275                 280                 285

Asn Asn Val Lys Pro Arg Lys Leu Arg Lys Asp
    290                 295
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<210> 51
<211> 1019
<212> DNA
<213> Homo sapiens

<400> 51
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ccagggaagg acctttcacc ttgactatat ggcattatgt catcacaagc tctgaggctt 120
ctcctttcca tcctgcgtgg acagctaaga cctcagtttt caatagcatc tagagcagtg 180
ggactcagct ggggtgattt cgccccccat ctccggggga atgtctgaag acaattttgg 240
ttacctcaat gagggagtgg aggaggatac agtgctacta ccaactagtg gataaaggcc 300
agggatgctg ctcaacctcc taccatgtac aggacgtctc cccattacaa ctacccaatc 360
cgaagtgtca actgtgtcag gactaagaaa ccctggtttt gagtagaaaa gggcctggaa 420
agaggggagc caacaaatct gtctgcttcc tcacattagt cattggcaaa taagcattct 480
gtctctttgg ctgctgcctc agcacagaga gccagaactc tatcgggcac caggataaca 540
tctctcagtg aacagagttg acaaggccta tgggaaatgc ctgatgggat tatcttcagc 600
ttgttgagct tctaagtttc tttcccttca ttctaccctg caagccaagt tctgtaagag 660
aaatgcctga gttctagctc aggttttctt actctgaatt tagatctcca gacccttcct 720
ggccacaatt caaattaagg caacaaacat ataccttcca tgaagcacac acagactttt 780
gaaagcaagg acaatgactg cttgaattga ggccttgagg aatgaagctt tgaaggaaaa 840
gaatactttg tttccagccc ccttcccaca ctcttcatgt gttaaccact gccttcctgg 900
accttggagc cacggtgact gtattacatg ttgttataga aaactgattt tagagttctg 960
atcgttcaag agaatgatta aatatacatt tcctacamaa aaaaaaaaaa aagtcgacg  1019
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<210> 52
<211> 1332
<212> DNA
<213> Homo sapiens

<400> 52
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ctttggcctc ggcctcccaa agtgcatgag ccaccatgcc tggcctgttt agttttgttt 120
caagttgaaa tacctttctt gtgttttcta attagaaaag taatatctac tcattgtaaa 180
aactcaaaca gtgcagaaat gtagaaagta gaaagtgtaa gtccctggtt gtcccttctg 240
cctgagcaca accactgctc acagtttgat gtatatcctt ccagagactc tcaaatttaa 300
gcaaataatt tttattacca tgtcttttta tttgaagacg tacatttgcc tccaaagttc 360
aacacaagtt caactgacca tatccttcca tgacctgaat agatgctatc ctttatcacg 420
atgttcaatt gcctttgaaa gagagtagtc caggtatatt cctgatcaaa atttggcatt 480
tttgatgata ctactctaca cagatcagac tcatgtgcag aatcgtgcct ggagagagag 540
gtttggttaa gacagagatt tctggaaaca ttcaaattgc aaatggaaac ttgaaaccca 600
caatctaatg aggaatgtac tggaaaaata atctgaagag ttgacaaatt gtgtactaga 660
ttgaacacat ggaatgcaat gccaatgaga ctttctgcac taaaacttat cctcatatgt 720
acaacaatga tgtgtgtatt atataacagt gatgtgtaca tttctgacac cccatacata 780
atatacacag tttgtataaa tgcatacatt taaaaatata tatgtacaat acagctaaca 840
taaaactgta gtacgcctga aggatattac tagtgcctaa tattgagtat gagtcactgc 900
gtgttcgcat caacttggaa gtgcagtaat tgttataaaa ttaatcagtg cagccaacat 960
tatttatgaa tcacatcttt gaaactgtgc agtagcatat acatatatat ttttaaataa 1020
cattttcac agttttccag agttactgtt gaaatctgca tcaccaaaaa aaaaaaaaag 1080
caagattttt ttaacaatgt agacactctt cagacccagt aatctgcgtg tgatttccta 1140
tttgtagatt cccaagagac tttagcagtc accagcctta atgcatgtac aggatattat 1200
tgtgacttaa tttatctgca gtttttaatc catgtgaaat tgggaatttt taaccgaact 1260
tggattaacc atgcctgcct ttctaaggtt gcaaatgtta cattaaatga tttatgttgt 1320
aaaaaaaaaa aa 1332

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (3)
<223> "Xaa" at position 3 can be any amino acid

<220>
<223> Description of Artificial Sequence: Ctyokine
receptor exctracellular motif found in many
species.

<400> 53
Trp Ser Xaa Trp Ser
1 5

<210> 54
<211> 2744
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(2387)

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ccagtgggcc cgtgtggaac caaacctgcg cgcgtggccg ggccgtggga caacgaggcc 120

gcggagacga aggcgca atg gcg agg aag tta tct gta atc ttg atc ctg 170
Met Ala Arg Lys Leu Ser Val Ile Leu Ile Leu
1 5 10

acc ttt gcc ctc tct gtc aca aat ccc ctt cat gaa cta aaa gca gct 218
Thr Phe Ala Leu Ser Val Thr Asn Pro Leu His Glu Leu Lys Ala Ala
15 20 25

gct ttc ccc cag acc act gag aaa att agt ccg aat tgg gaa tct ggc 266
Ala Phe Pro Gln Thr Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly
30 35 40

att aat gtt gac ttg gca att tcc aca cgg caa tat cat cta caa cag 314
Ile Asn Val Asp Leu Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln
45 50 55

ctt ttc tac cgc tat gga gaa aat aat tct ttg tca gtt gaa ggg ttc 362
Leu Phe Tyr Arg Tyr Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe
60 65 70 75

aga aaa tta ctt caa aat ata ggc ata gat aag att aaa aga atc cat 410
Arg Lys Leu Leu Gln Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His
80 85 90

ata cac cat gac cac gac cat cac tca gac cac gag cat cac tca gac 458
Ile His His Asp His Asp His His Ser Asp His Glu His His Ser Asp
95 100 105

cat gag cgt cac tca gac cat gag cat cac tca gac cac gag cat cac 506
His Glu Arg His Ser Asp His Glu His His Ser Asp His Glu His His
110 115 120

tct gac cat aat cat gct gct tct ggt aaa aat aag cga aaa gct ctt 554
Ser Asp His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala Leu
125 130 135

tgc cca gac cat gac tca gat agt tca ggt aaa gat cct aga aac agc 602
Cys Pro Asp His Asp Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn Ser
140 145 150 155

cag ggg aaa gga gct cac cga cca gaa cat gcc agt ggt aga agg aat 650
Gln Gly Lys Gly Ala His Arg Pro Glu His Ala Ser Gly Arg Arg Asn

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                160                 165                 170

gtc aag gac agt gtt agt gct agt gaa gtg acc tca act gtg tac aac   698
Val Lys Asp Ser Val Ser Ala Ser Glu Val Thr Ser Thr Val Tyr Asn
            175                 180                 185

act gtc tct gaa gga act cac ttt cta gag aca ata gag act cca aga   746
Thr Val Ser Glu Gly Thr His Phe Leu Glu Thr Ile Glu Thr Pro Arg
        190                 195                 200

cct gga aaa ctc ttc ccc aaa gat gta agc agc tcc act cca ccc agt   794
Pro Gly Lys Leu Phe Pro Lys Asp Val Ser Ser Ser Thr Pro Pro Ser
    205                 210                 215

gtc aca tca aag agc cgg gtg agc cgg ctg gct ggt agg aaa aca aat   842
Val Thr Ser Lys Ser Arg Val Ser Arg Leu Ala Gly Arg Lys Thr Asn
220                 225                 230                 235

gaa tct gtg agt gag ccc cga aaa ggc ttt atg tat tcc aga aac aca   890
Glu Ser Val Ser Glu Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn Thr
                240                 245                 250

aat gaa aat cct cag gag tgt ttc aat gca tca aag cta ctg aca tct   938
Asn Glu Asn Pro Gln Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr Ser
            255                 260                 265

cat ggc atg ggc atc cag gtt ccg ctg aat gca aca gag ttc aac tat   986
His Gly Met Gly Ile Gln Val Pro Leu Asn Ala Thr Glu Phe Asn Tyr
        270                 275                 280

ctc tgt cca gcc atc atc aac caa att gat gct aga tct tgt ctg att   1034
Leu Cys Pro Ala Ile Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu Ile
    285                 290                 295

cat aca agt gaa aag aag gct gaa atc cct cca aag acc tat tca tta   1082
His Thr Ser Glu Lys Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser Leu
300                 305                 310                 315

caa ata gcc tgg gtt ggt ggt ttt ata gcc att tcc atc atc agt ttc   1130
Gln Ile Ala Trp Val Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser Phe
                320                 325                 330

ctg tct ctg ctg ggg gtt atc tta gtg cct ctc atg aat cgg gtg ttt   1178
Leu Ser Leu Leu Gly Val Ile Leu Val Pro Leu Met Asn Arg Val Phe
            335                 340                 345

ttc aaa ttt ctc ctg agt ttc ctt gtg gca ctg gcc gtt ggg act ttg   1226
Phe Lys Phe Leu Leu Ser Phe Leu Val Ala Leu Ala Val Gly Thr Leu
        350                 355                 360

agt ggt gat gct ttt tta cac ctt ctt cca cat tct cat gca agt cac   1274
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Ser Gly Asp Ala Phe Leu His Leu Leu Pro His Ser His Ala Ser His
    365                 370                 375

cac cat agt cat agc cat gaa gaa cca gca atg gaa atg aaa aga gga   1322
His His Ser His Ser His Glu Glu Pro Ala Met Glu Met Lys Arg Gly
380                 385                 390                 395

cca ctt ttc agt cat ctg tct tct caa aac ata gaa gaa agt gcc tat   1370
Pro Leu Phe Ser His Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala Tyr
                400                 405                 410

ttt gat tcc acg tgg aag ggt cta aca gct cta gga ggc ctg tat ttc   1418
Phe Asp Ser Thr Trp Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr Phe
            415                 420                 425

atg ttt ctt gtt gaa cat gtc ctc aca ttg atc aaa caa ttt aaa gat   1466
Met Phe Leu Val Glu His Val Leu Thr Leu Ile Lys Gln Phe Lys Asp
        430                 435                 440

aag aag aaa aag aat cag aag aaa cct gaa aat gat gat gat gtg gag   1514
Lys Lys Lys Lys Asn Gln Lys Lys Pro Glu Asn Asp Asp Asp Val Glu
    445                 450                 455

att aag aag cag ttg tcc aag tat gaa tct caa ctt tca aca aat gag   1562
Ile Lys Lys Gln Leu Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn Glu
460                 465                 470                 475

gag aaa gta gat aca gat gat cga act gaa ggc tat tta cga gca gac   1610
Glu Lys Val Asp Thr Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala Asp
                480                 485                 490

tca caa gag ccc tcc cac ttt gat tct cag cag cct gca gtc ttg gaa   1658
Ser Gln Glu Pro Ser His Phe Asp Ser Gln Gln Pro Ala Val Leu Glu
            495                 500                 505

gaa gaa gag gtc atg ata gct cat gct cat cca cag gaa gtc tac aat   1706
Glu Glu Glu Val Met Ile Ala His Ala His Pro Gln Glu Val Tyr Asn
        510                 515                 520

gaa tat gta ccc aga ggg tgc aag aat aaa tgc cat tca cat ttc cac   1754
Glu Tyr Val Pro Arg Gly Cys Lys Asn Lys Cys His Ser His Phe His
    525                 530                 535

gat aca ctc ggc cag tca gac gat ctc att cac cac cat cat gac tac   1802
Asp Thr Leu Gly Gln Ser Asp Asp Leu Ile His His His His Asp Tyr
540                 545                 550                 555

cat cat att ctc cat cat cac cac cac caa aac cac cat cct cac agt   1850
His His Ile Leu His His His His His Gln Asn His His Pro His Ser
                560                 565                 570
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cac agc cag cgc tac tct cgg gag gag ctg aaa gat gcc ggc gtc gcc   1898
His Ser Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val Ala
            575                 580                 585

act ttg gcc tgg atg gtg ata atg ggt gat ggc ctg cac aat ttc agc   1946
Thr Leu Ala Trp Met Val Ile Met Gly Asp Gly Leu His Asn Phe Ser
        590                 595                 600

gat ggc cta gca att ggt gct gct ttt act gaa ggc tta tca agt ggt   1994
Asp Gly Leu Ala Ile Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser Gly
    605                 610                 615

tta agt act tct gtt gct gtg ttc tgt cat gag ttg cct cat gaa tta   2042
Leu Ser Thr Ser Val Ala Val Phe Cys His Glu Leu Pro His Glu Leu
620                 625                 630                 635

ggt gac ttt gct gtt cta cta aag gct ggc atg acc gtt aag cag gct   2090
Gly Asp Phe Ala Val Leu Leu Lys Ala Gly Met Thr Val Lys Gln Ala
                640                 645                 650

gtc ctt tat aat gca ttg tca gcc atg ctg gcg tat ctt gga atg gca   2138
Val Leu Tyr Asn Ala Leu Ser Ala Met Leu Ala Tyr Leu Gly Met Ala
            655                 660                 665

aca gga att ttc att ggt cat tat gct gaa aat gtt tct atg tgg ata   2186
Thr Gly Ile Phe Ile Gly His Tyr Ala Glu Asn Val Ser Met Trp Ile
        670                 675                 680

ttt gca ctt act gct ggc tta ttc atg tat gtt gct ctg gtt gat atg   2234
Phe Ala Leu Thr Ala Gly Leu Phe Met Tyr Val Ala Leu Val Asp Met
    685                 690                 695

gta cct gaa atg ctg cac aat gat gct agt gac cat gga tgt agc cgc   2282
Val Pro Glu Met Leu His Asn Asp Ala Ser Asp His Gly Cys Ser Arg
700                 705                 710                 715

tgg ggg tat ttc ttt tta cag aat gct ggg atg ctt ttg ggt ttt gga   2330
Trp Gly Tyr Phe Phe Leu Gln Asn Ala Gly Met Leu Leu Gly Phe Gly
                720                 725                 730

att atg tta ctt att tcc ata ttt gaa cat aaa atc gtg ttt cgt ata   2378
Ile Met Leu Leu Ile Ser Ile Phe Glu His Lys Ile Val Phe Arg Ile
            735                 740                 745

aat ttc tag ttaaggttta aatgctagag tagcttaaaa agttgtcata           2427
Asn Phe

gtttcagtag gtcataggga gatgagtttg tatgctgtac tatgcagcgt ttaaagttag 2487

tgggttttgt gatttttgta ttgaatattg ctgtctgtta caaagtcagt taaaggtacg 2547
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ttttaatatt taagttattc tatcttggag ataaaatctg tatgtgcaat tcaccggtat 2607

taccagttta ttatgtaaac aagagatttg gcatgacatg ttctgtatgt ttcagggaaa 2667

aatgtcttta atgctttttc aagaactaac acagttattc ctatactgga ttttaggtct 2727

ctgaagaact gctggtg 2744

<210> 55
<211> 749
<212> PRT
<213> Homo sapiens

<400> 55

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Met Ala Arg Lys Leu Ser Val Ile Leu Ile Leu Thr Phe Ala Leu Ser
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Val Thr Asn Pro Leu His Glu Leu Lys Ala Ala Ala Phe Pro Gln Thr
             20                  25                  30
Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly Ile Asn Val Asp Leu
         35                  40                  45
Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln Leu Phe Tyr Arg Tyr
     50                  55                  60
Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe Arg Lys Leu Leu Gln
 65                  70                  75                  80
Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His Ile His His Asp His
                 85                  90                  95
Asp His His Ser Asp His Glu His His Ser Asp His Glu Arg His Ser
            100                 105                 110
Asp His Glu His His Ser Asp His Glu His His Ser Asp His Asn His
        115                 120                 125
Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala Leu Cys Pro Asp His Asp
    130                 135                 140
Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn Ser Gln Gly Lys Gly Ala
145                 150                 155                 160
His Arg Pro Glu His Ala Ser Gly Arg Arg Asn Val Lys Asp Ser Val
                165                 170                 175
Ser Ala Ser Glu Val Thr Ser Thr Val Tyr Asn Thr Val Ser Glu Gly
            180                 185                 190
Thr His Phe Leu Glu Thr Ile Glu Thr Pro Arg Pro Gly Lys Leu Phe
        195                 200                 205
Pro Lys Asp Val Ser Ser Ser Thr Pro Pro Ser Val Thr Ser Lys Ser
    210                 215                 220
Arg Val Ser Arg Leu Ala Gly Arg Lys Thr Asn Glu Ser Val Ser Glu
225                 230                 235                 240
Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn Thr Asn Glu Asn Pro Gln
                245                 250                 255
Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr Ser His Gly Met Gly Ile
            260                 265                 270
Gln Val Pro Leu Asn Ala Thr Glu Phe Asn Tyr Leu Cys Pro Ala Ile
        275                 280                 285
```

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Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu Ile His Thr Ser Glu Lys
    290                 295                 300
Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser Leu Gln Ile Ala Trp Val
305                 310                 315                 320
Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser Phe Leu Ser Leu Leu Gly
                325                 330                 335
Val Ile Leu Val Pro Leu Met Asn Arg Val Phe Phe Lys Phe Leu Leu
            340                 345                 350
Ser Phe Leu Val Ala Leu Ala Val Gly Thr Leu Ser Gly Asp Ala Phe
        355                 360                 365
Leu His Leu Leu Pro His Ser His Ala Ser His His His Ser His Ser
    370                 375                 380
His Glu Glu Pro Ala Met Glu Met Lys Arg Gly Pro Leu Phe Ser His
385                 390                 395                 400
Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala Tyr Phe Asp Ser Thr Trp
                405                 410                 415
Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr Phe Met Phe Leu Val Glu
            420                 425                 430
His Val Leu Thr Leu Ile Lys Gln Phe Lys Asp Lys Lys Lys Lys Asn
        435                 440                 445
Gln Lys Lys Pro Glu Asn Asp Asp Asp Val Glu Ile Lys Lys Gln Leu
    450                 455                 460
Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn Glu Glu Lys Val Asp Thr
465                 470                 475                 480
Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala Asp Ser Gln Glu Pro Ser
                485                 490                 495
His Phe Asp Ser Gln Gln Pro Ala Val Leu Glu Glu Glu Glu Val Met
            500                 505                 510
Ile Ala His Ala His Pro Gln Glu Val Tyr Asn Glu Tyr Val Pro Arg
        515                 520                 525
Gly Cys Lys Asn Lys Cys His Ser His Phe His Asp Thr Leu Gly Gln
    530                 535                 540
Ser Asp Asp Leu Ile His His His His Asp Tyr His His Ile Leu His
545                 550                 555                 560
His His His His Gln Asn His His Pro His Ser His Ser Gln Arg Tyr
                565                 570                 575
Ser Arg Glu Glu Leu Lys Asp Ala Gly Val Ala Thr Leu Ala Trp Met
            580                 585                 590
Val Ile Met Gly Asp Gly Leu His Asn Phe Ser Asp Gly Leu Ala Ile
        595                 600                 605
Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser Gly Leu Ser Thr Ser Val
    610                 615                 620
Ala Val Phe Cys His Glu Leu Pro His Glu Leu Gly Asp Phe Ala Val
625                 630                 635                 640
Leu Leu Lys Ala Gly Met Thr Val Lys Gln Ala Val Leu Tyr Asn Ala
                645                 650                 655
Leu Ser Ala Met Leu Ala Tyr Leu Gly Met Ala Thr Gly Ile Phe Ile
            660                 665                 670
Gly His Tyr Ala Glu Asn Val Ser Met Trp Ile Phe Ala Leu Thr Ala
        675                 680                 685
Gly Leu Phe Met Tyr Val Ala Leu Val Asp Met Val Pro Glu Met Leu
```

```
    690                 695                 700
His Asn Asp Ala Ser Asp His Gly Cys Ser Arg Trp Gly Tyr Phe Phe
705                 710                 715                 720
Leu Gln Asn Ala Gly Met Leu Leu Gly Phe Gly Ile Met Leu Leu Ile
                725                 730                 735
Ser Ile Phe Glu His Lys Ile Val Phe Arg Ile Asn Phe
            740                 745
```

<210> 56
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (190)
<223> "n" at position 190 can be any base

<400> 56
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ttttttttac tgtgaaattc taaaatcata tttattcacc aattcacaga aagtgtcata 60
acgaccacca acatgaatca gtttgtaggc atttacaagc cacagctgaa aataaaaatc 120
tgtctgtgtt gaataggcat ttaacaaatt acttgaaaac tgcaagaatc ataattatta 180
taaatttaan gtttgtgatt caaacatggg taagatcaca gtcatgggga gaagcccaac 240
agattcctgt gatgatcctt attttcttcc tatatcttta tatacatagg agg        293
```

<210> 57
<211> 2053
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (85)..(1347)

<400> 57
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ccggctcgcg ccctccgggc ccagcctccc gagccttcgg agcgggcgcc gtcccagccc 60

agctccgggg aaacgcgagc cgcg atg cct ggg ggg tgc tcc cgg ggc ccc    111
                          Met Pro Gly Gly Cys Ser Arg Gly Pro
                            1               5

gcc gcc ggg gac ggg cgt ctg cgg ctg gcg cga cta gcg ctg gta ctc   159
Ala Ala Gly Asp Gly Arg Leu Arg Leu Ala Arg Leu Ala Leu Val Leu
 10                  15                  20                  25

ctg ggc tgg gtc tcc tcg tct tct ccc acc tcc tcg gca tcc tcc ttc   207
Leu Gly Trp Val Ser Ser Ser Ser Pro Thr Ser Ser Ala Ser Ser Phe
                30                  35                  40
```

```
tcc tcc tcg gcg ccg ttc ctg gct tcc gcc gtg tcc gcc cag ccc ccg   255
Ser Ser Ser Ala Pro Phe Leu Ala Ser Ala Val Ser Ala Gln Pro Pro
            45                  50                  55

ctg ccg gac cag tgc ccc gcg ctg tgc gag tgc tcc gag gca gcg cgc   303
Leu Pro Asp Gln Cys Pro Ala Leu Cys Glu Cys Ser Glu Ala Ala Arg
        60                  65                  70

aca gtc aag tgc gtt aac cgc aat ctg acc gag gtg ccc acg gac ctg   351
Thr Val Lys Cys Val Asn Arg Asn Leu Thr Glu Val Pro Thr Asp Leu
    75                  80                  85

ccc gcc tac gtg cgc aac ctc ttc ctt acc ggc aac cag ctg gcc gtg   399
Pro Ala Tyr Val Arg Asn Leu Phe Leu Thr Gly Asn Gln Leu Ala Val
90                  95                  100                 105

ctc cct gcc ggc gcc ttc gcc cgc cgg ccg ccg ctg gcg gag ctg gcc   447
Leu Pro Ala Gly Ala Phe Ala Arg Arg Pro Pro Leu Ala Glu Leu Ala
                110                 115                 120

gcg ctc aac ctc agc ggc agc cgc ctg gac gag gtg cgc gcg ggc gcc   495
Ala Leu Asn Leu Ser Gly Ser Arg Leu Asp Glu Val Arg Ala Gly Ala
            125                 130                 135

ttc gag cat ctg ccc agc ctg cgc cag ctc gac ctc agc cac aac cca   543
Phe Glu His Leu Pro Ser Leu Arg Gln Leu Asp Leu Ser His Asn Pro
        140                 145                 150

ctg gcc gac ctc agt ccc ttc gct ttc tcg ggc agc aat gcc agc gtc   591
Leu Ala Asp Leu Ser Pro Phe Ala Phe Ser Gly Ser Asn Ala Ser Val
    155                 160                 165

tcg gcc ccc agt ccc ctt gtg gaa ctg atc ctg aac cac atc gtg ccc   639
Ser Ala Pro Ser Pro Leu Val Glu Leu Ile Leu Asn His Ile Val Pro
170                 175                 180                 185

cct gaa gat gag cgg cag aac cgg agc ttc gag ggc atg gtg gtg gcg   687
Pro Glu Asp Glu Arg Gln Asn Arg Ser Phe Glu Gly Met Val Val Ala
                190                 195                 200

gcc ctg ctg gcg ggc cgt gca ctg cag ggg ctc cgc cgc ttg gag ctg   735
Ala Leu Leu Ala Gly Arg Ala Leu Gln Gly Leu Arg Arg Leu Glu Leu
            205                 210                 215

gcc agc aac cac ttc ctt tac ctg ccg cgg gat gtg ctg gcc caa ctg   783
Ala Ser Asn His Phe Leu Tyr Leu Pro Arg Asp Val Leu Ala Gln Leu
        220                 225                 230

ccc agc ctc agg cac ctg gac tta agt aat aat tcg ctg gtg agc ctg   831
Pro Ser Leu Arg His Leu Asp Leu Ser Asn Asn Ser Leu Val Ser Leu
    235                 240                 245
```

```
acc tac gtg tcc ttc cgc aac ctg aca cat cta gaa agc ctc cac ctg   879
Thr Tyr Val Ser Phe Arg Asn Leu Thr His Leu Glu Ser Leu His Leu
250                 255                 260                 265

gag gac aat gcc ctc aag gtc ctt cac aat ggc acc ctg gct gag ttg   927
Glu Asp Asn Ala Leu Lys Val Leu His Asn Gly Thr Leu Ala Glu Leu
                270                 275                 280

caa ggt cta ccc cac att agg gtt ttc ctg gac aac aat ccc tgg gtc   975
Gln Gly Leu Pro His Ile Arg Val Phe Leu Asp Asn Asn Pro Trp Val
            285                 290                 295

tgc gac tgc cac atg gca gac atg gtg acc tgg ctc aag gaa aca gag   1023
Cys Asp Cys His Met Ala Asp Met Val Thr Trp Leu Lys Glu Thr Glu
        300                 305                 310

gta gtg cag ggc aaa gac cgg ctc acc tgt gca tat ccg gaa aaa atg   1071
Val Val Gln Gly Lys Asp Arg Leu Thr Cys Ala Tyr Pro Glu Lys Met
    315                 320                 325

agg aat cgg gtc ctc ttg gaa ctc aac agt gct gac ctg gac tgt gac   1119
Arg Asn Arg Val Leu Leu Glu Leu Asn Ser Ala Asp Leu Asp Cys Asp
330                 335                 340                 345

ccg att ctt ccc cca tcc ctg caa acc tct tat gtc ttc ctg ggt att   1167
Pro Ile Leu Pro Pro Ser Leu Gln Thr Ser Tyr Val Phe Leu Gly Ile
                350                 355                 360

gtt tta gcc ctg ata ggc gct att ttc ctc ctg gtt ttg tat ttg aac   1215
Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu Tyr Leu Asn
            365                 370                 375

cgc aag ggg ata aaa aag tgg atg cat aac atc aga gat gcc tgc agg   1263
Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp Ala Cys Arg
        380                 385                 390

gat cac atg gaa ggg tat cat tac aga tat gaa atc aat gcg gac ccc   1311
Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn Ala Asp Pro
    395                 400                 405

aga tta aca aac ctc agt tct aac tcg gat gtc tga gaaatattag        1357
Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
410                 415                 420

aggacagacc aaggacaact ctgcatgaga tgtagactta agctttatcc ctactaggct 1417

tgctccactt tcatcctcca ctatagatac aacggacttt gactaaaagc agtgaagggg 1477

atttgcttcc ttgttatgta aagtttctcg gtgtgttctg ttaatgtaag acgatgaaca 1537

gttgtgtata gtgttttacc ctcttctttt tcttggaact cctcaacacg tatggaggga 1597
```

```
tttttcaggt ttcagcatga acatgggctt cttgctgtct gtctctctct cagtacagtt 1657

caaggtgtag caagtgtacc cacacagata gcattcaaca aaagctgcct caacttttc 1717

gagaaaaata ctttattcat aaatatcagt tttattctca tgtacctaag ttgtggagaa 1777

aataattgca tcctataaac tgcctgcaga cgttagcagg ctcttcaaaa taactccatg 1837

gtgcacagga gcacctgcat ccaagagcat gcttacattt tactgttctg catattacaa 1897

aaaataactt gcaacttcat aacttctttg acaaagtaaa ttacttttt gattgcagtt 1957

tatatgaaaa tgtactgatt ttttttaat aaactgcatc gagatccaac cgactgaatt 2017

gttaaaaaaa aaaaaaaata aagattctta aaagaa                          2053
```

<210> 58
<211> 420
<212> PRT
<213> Homo sapiens

<400> 58

```
Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg Leu
  1               5                  10                  15
Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
             20                  25                  30
Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu
         35                  40                  45
Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala
     50                  55                  60
Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
 65                  70                  75                  80
Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn Leu
                 85                  90                  95
Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
            100                 105                 110
Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser
        115                 120                 125
Arg Leu Asp Glu Val Arg Ala Gly Ala Phe Glu His Leu Pro Ser Leu
    130                 135                 140
Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Asp Leu Ser Pro Phe
145                 150                 155                 160
Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val
                165                 170                 175
Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln Asn
            180                 185                 190
Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Leu Ala Gly Arg Ala
        195                 200                 205
Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
    210                 215                 220
```

```
Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp
225                 230                 235                 240
Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
                245                 250                 255
Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
            260                 265                 270
Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile Arg
        275                 280                 285
Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
    290                 295                 300
Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp Arg
305                 310                 315                 320
Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
                325                 330                 335
Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
            340                 345                 350
Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly Ala
        355                 360                 365
Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp
    370                 375                 380
Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr His
385                 390                 395                 400
Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser
                405                 410                 415
Asn Ser Asp Val
            420
```

<210> 59
<211> 232
<212> DNA
<213> Homo sapiens

<400> 59
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tttttaatta tactctttta ttgaaagaaa aaacaataca atggacttta aaaagctaca 60
tttgttatgg ttcataagga cagaggttta cacaggtttt atatatgtac acactgacaa 120
tactatatca caacatcaga ggcaccattt ttgccacaga attaggtaat gaataaaact 180
tctccaaatt aatctgttta aaaaatatct aaaatggtac agtatatttg ag         232
```

<210> 60
<211> 281
<212> DNA
<213> Homo sapiens

<400> 60
```
taccaaaata tctgtattat ctataaaaat tgaactctaa tgagtcactg atacgggagg 60
cagcaatacc cgactgtgct gacatgcaga aggaagacag ctctgtccca ccaaccctat 120
agcagaacat ttgtattgag tggcacgtgg gctgagtcat ttgtaaggtc tcaaaaacct 180
ggacactttg gaacgtagca atcggatgaa cgatcttgga aacatctctc gggactcctg 240
```

```
ggctgtgtac ttgaaatagt tctggggatg ggccaggaca t                          281


<210> 61
<211> 3085
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (256)..(3012)

<400> 61
gagcagccaa aaggcccgcg gagtcgcgct gggccgcccc ggcgcagctg aaccgggggc 60

cgcgcctgcc aggccgacgg gtctggccca gcctggcgcc aaggggttcg tgcgctgtgg 120

agacgcggag ggtcgaggcg gcgcggcctg agtgaaaccc aatggaaaaa gcatgacatt 180

tagaagtaga agacttagct tcaaatccct actccttcac ttactaattt tgtgatttgg 240

aaatatccgc gcaag atg ttg acg ttg cag act tgg gta gtg caa gcc ttg  291
                Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu
                  1               5                  10

ttt att ttc ctc acc act gaa tct aca ggt gaa ctt cta gat cca tgt   339
Phe Ile Phe Leu Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys
         15                  20                  25

ggt tat atc agt cct gaa tct cca gtt gta caa ctt cat tct aat ttc   387
Gly Tyr Ile Ser Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe
     30                  35                  40

act gca gtt tgt gtg cta aag gaa aaa tgt atg gat tat ttt cat gta   435
Thr Ala Val Cys Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val
 45                  50                  55                  60

aat gct aat tac att gtc tgg aaa aca aac cat ttt act att cct aag   483
Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys
                65                  70                  75

gag caa tat act atc ata aac aga aca gca tcc agt gtc acc ttt aca   531
Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr
            80                  85                  90

gat ata gct tca tta aat att cag ctc act tgc aac att ctt aca ttc   579
Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe
        95                  100                 105

gga cag ctt gaa cag aat gtt tat gga atc aca ata att tca ggc ttg   627
Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu
```

```
    110                 115                 120

cct cca gaa aaa cct aaa aat ttg agt tgc att gtg aac gag ggg aag   675
Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys
125                 130                 135                 140

aaa atg agg tgt gag tgg gat ggt gga agg gaa aca cac ttg gag aca   723
Lys Met Arg Cys Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr
                145                 150                 155

aac ttc act tta aaa tct gaa tgg gca aca cac aag ttt gct gat tgc   771
Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys
            160                 165                 170

aaa gca aaa cgt gac acc ccc acc tca tgc act gtt gat tat tct act   819
Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr
        175                 180                 185

gtg tat ttt gtc aac att gaa gtc tgg gta gaa gca gag aat gcc ctt   867
Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu
    190                 195                 200

ggg aag gtt aca tca gat cat atc aat ttt gat cct gta tat aaa gtg   915
Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val
205                 210                 215                 220

aag ccc aat ccg cca cat aat tta tca gtg atc aac tca gag gaa ctg   963
Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu
                225                 230                 235

tct agt atc tta aaa ttg aca tgg acc aac cca agt att aag agt gtt   1011
Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val
            240                 245                 250

ata ata cta aaa tat aac att caa tat agg acc aaa gat gcc tca act   1059
Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr
        255                 260                 265

tgg agc cag att cct cct gaa gac aca gca tcc acc cga tct tca ttc   1107
Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe
    270                 275                 280

act gtc caa gac ctt aaa cct ttt aca gaa tat gtg ttt agg att cgc   1155
Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg
285                 290                 295                 300

tgt atg aag gaa gat ggt aag gga tac tgg agt gac tgg agt gaa gaa   1203
Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu
                305                 310                 315

gca agt ggg atc acc tat gaa gat aga cca tct aaa gca cca agt ttc   1251
```

```
Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe
            320                 325                 330

tgg tat aaa ata gat cca tcc cat act caa ggc tac aga act gta caa   1299
Trp Tyr Lys Ile Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln
        335                 340                 345

ctc gtg tgg aag aca ttg cct cct ttt gaa gcc aat gga aaa atc ttg   1347
Leu Val Trp Lys Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu
    350                 355                 360

gat tat gaa gtg act ctc aca aga tgg aaa tca cat tta caa aat tac   1395
Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr
365                 370                 375                 380

aca gtt aat gcc aca aaa ctg aca gta aat ctc aca aat gat cgc tat   1443
Thr Val Asn Ala Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr
                385                 390                 395

cta gca acc cta aca gta aga aat ctt gtt ggc aaa tca gat gca gct   1491
Leu Ala Thr Leu Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala
            400                 405                 410

gtt tta act atc cct gcc tgt gac ttt caa gct act cac cct gta atg   1539
Val Leu Thr Ile Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met
        415                 420                 425

gat ctt aaa gca ttc ccc aaa gat aac atg ctt tgg gtg gaa tgg act   1587
Asp Leu Lys Ala Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr
    430                 435                 440

act cca agg gaa tct gta aag aaa tat ata ctt gag tgg tgt gtg tta   1635
Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu
445                 450                 455                 460

tca gat aaa gca ccc tgt atc aca gac tgg caa caa gaa gat ggt acc   1683
Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr
                465                 470                 475

gtg cat cgc acc tat tta aga ggg aac tta gca gag agc aaa tgc tat   1731
Val His Arg Thr Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr
            480                 485                 490

ttg ata aca gtt act cca gta tat gct gat gga cca gga agc cct gaa   1779
Leu Ile Thr Val Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu
        495                 500                 505

tcc ata aag gca tac ctt aaa caa gct cca cct tcc aaa gga cct act   1827
Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr
    510                 515                 520
```

```
gtt cgg aca aaa aaa gta ggg aaa aac gaa gct gtc tta gag tgg gac   1875
Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp
525                 530                 535                 540

caa ctt cct gtt gat gtt cag aat gga ttt atc aga aat tat act ata   1923
Gln Leu Pro Val Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile
                545                 550                 555

ttt tat aga acc atc att gga aat gaa act gct gtg aat gtg gat tct   1971
Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser
            560                 565                 570

tcc cac aca gaa tat aca ttg tcc tct ttg act agt gac aca ttg tac   2019
Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr
        575                 580                 585

atg gta cga atg gca gca tac aca gat gaa ggt ggg aag gat ggt cca   2067
Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro
    590                 595                 600

gaa ttc act ttt act acc cca aag ttt gct caa gga gaa att gaa gcc   2115
Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala
605                 610                 615                 620

ata gtc gtg cct gtt tgc tta gca ttc cta ttg aca act ctt ctg gga   2163
Ile Val Val Pro Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly
                625                 630                 635

gtg ctg ttc tgc ttt aat aag cga gac cta att aaa aaa cac atc tgg   2211
Val Leu Phe Cys Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp
            640                 645                 650

cct aat gtt cca gat cct tca aag agt cat att gcc cag tgg tca cct   2259
Pro Asn Val Pro Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro
        655                 660                 665

cac act cct cca agg cac aat ttt aat tca aaa gat caa atg tat tca   2307
His Thr Pro Pro Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser
    670                 675                 680

gat ggc aat ttc act gat gta agt gtt gtg gaa ata gaa gca aat gac   2355
Asp Gly Asn Phe Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp
685                 690                 695                 700

aaa aag cct ttt cca gaa gat ctg aaa tca ttg gac ctg ttc aaa aag   2403
Lys Lys Pro Phe Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys
                705                 710                 715

gaa aaa att aat act gaa gga cac agc agt ggt att ggg ggg tct tca   2451
Glu Lys Ile Asn Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser
            720                 725                 730
```

```
tgc atg tca tct tct agg cca agc att tct agc agt gat gaa aat gaa   2499
Cys Met Ser Ser Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu
        735                 740                 745

tct tca caa aac act tcg agc act gtc cag tat tct acc gtg gta cac   2547
Ser Ser Gln Asn Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His
    750                 755                 760

agt ggc tac aga cac caa gtt ccg tca gtc caa gtc ttc tca aga tcc   2595
Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser
765                 770                 775                 780

gag tct acc cag ccc ttg tta gat tca gag gag cgg cca gaa gat cta   2643
Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu
                785                 790                 795

caa tta gta gat cat gta gat ggc ggt gat ggt att ttg ccc agg caa   2691
Gln Leu Val Asp His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln
            800                 805                 810

cag tac ttc aaa cag aac tgc agt cag cat gaa tcc agt cca gat att   2739
Gln Tyr Phe Lys Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile
        815                 820                 825

tca cat ttt gaa agg tca aag caa gtt tca tca gtc aat gag gaa gat   2787
Ser His Phe Glu Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp
    830                 835                 840

ttt gtt aga ctt aaa cag cag att tca gat cat att tca caa tcc tgt   2835
Phe Val Arg Leu Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys
845                 850                 855                 860

gga tct ggg caa atg aaa atg ttt cag gaa gtt tct gca gca gat gct   2883
Gly Ser Gly Gln Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala
                865                 870                 875

ttt ggt cca ggt act gag gga caa gta gaa aga ttt gaa aca gtt ggc   2931
Phe Gly Pro Gly Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly
            880                 885                 890

atg gag gct gcg act gat gaa ggc atg cct aaa agt tac tta cca cag   2979
Met Glu Ala Ala Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln
        895                 900                 905

act gta cgg caa ggc ggc tac atg cct cag tga aggactagta gttcctgcta 3032
Thr Val Arg Gln Gly Gly Tyr Met Pro Gln
    910                 915

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<400> 62
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Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
35 40 45
Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
50 55 60
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65 70 75 80
Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
85 90 95
Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
100 105 110
Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
115 120 125
Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
130 135 140
Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145 150 155 160
Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
165 170 175
Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
180 185 190
Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
195 200 205
Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
210 215 220
Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225 230 235 240
Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
245 250 255
Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
260 265 270
Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
275 280 285
Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
290 295 300
Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305 310 315 320
Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
325 330 335
Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
340 345 350
Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val

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        355                 360                 365
Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
    370                 375                 380
Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
385                 390                 395                 400
Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
                405                 410                 415
Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
            420                 425                 430
Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
        435                 440                 445
Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
    450                 455                 460
Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465                 470                 475                 480
Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
                485                 490                 495
Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
            500                 505                 510
Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
        515                 520                 525
Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
    530                 535                 540
Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545                 550                 555                 560
Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
                565                 570                 575
Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
            580                 585                 590
Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
        595                 600                 605
Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
    610                 615                 620
Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
625                 630                 635                 640
Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
                645                 650                 655
Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
            660                 665                 670
Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe
        675                 680                 685
Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp Lys Lys Pro Phe
    690                 695                 700
Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
705                 710                 715                 720
Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
                725                 730                 735
Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
            740                 745                 750
Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
        755                 760                 765
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His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
    770                 775                 780
Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
785                 790                 795                 800
His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys
                805                 810                 815
Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
            820                 825                 830
Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
        835                 840                 845
Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Gln
    850                 855                 860
Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala Phe Gly Pro Gly
865                 870                 875                 880
Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly Met Glu Ala Ala
                885                 890                 895
Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln
            900                 905                 910
Gly Gly Tyr Met Pro Gln
        915
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